



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/684,883

DATE: 07/30/2002

TIME: 14:21:00

Input Set : N:\Crif3\RULE60\09684883.raw  
Output Set: N:\CRF3\07302002\I684883.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Brodeur, Bernard R  
6 Martin, Denis  
7 Hamel, Josee  
8 Rioux, Clement

10 (ii) TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
11 OF NEISSERIA MENINGITIDIS

13 (iii) NUMBER OF SEQUENCES: 30

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Foley & Lardner  
17 (B) STREET: 3000 K Street, N.W., Suite 500  
18 (C) CITY: Washington  
19 (D) STATE: D.C.  
20 (E) COUNTRY: USA  
21 (F) ZIP: 20007-5109

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/684,883  
C--> 31 (B) FILING DATE: 06-Oct-2000

42 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/08/913,362  
35 (B) FILING DATE: 13-NOV-1997  
39 (A) APPLICATION NUMBER: US 08/406,362  
40 (B) FILING DATE: 17-MAR-1995  
43 (A) APPLICATION NUMBER: US 60/001,983  
44 (B) FILING DATE: 04-AUG-1995

46 (viii) ATTORNEY/AGENT INFORMATION:

47 (A) NAME: Bent, Stephen A.  
48 (B) REGISTRATION NUMBER: 29,768  
49 (C) REFERENCE/DOCKET NUMBER: 047998/0128

51 (ix) TELECOMMUNICATION INFORMATION:

52 (A) TELEPHONE: (202)672-5300  
53 (B) TELEFAX: (202)672-5399  
54 (C) TELEX: 904136

57 (2) INFORMATION FOR SEQ ID NO: 1:

59 (i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 830 base pairs  
61 (B) TYPE: nucleic acid

ENTERED

RECEIVED

AUG 06 2002

TECH CENTER 1600/2900

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```

62      (C) STRANDEDNESS: double
63      (D) TOPOLOGY: linear
65      (ii) MOLECULE TYPE: DNA (genomic)
67      (iii) HYPOTHETICAL: NO
69      (iv) ANTI-SENSE: NO
71      (vi) ORIGINAL SOURCE:
72          (A) ORGANISM: Neisseria meningitidis
73          (B) STRAIN: 608B
75      (ix) FEATURE:
76          (A) NAME/KEY: CDS
77          (B) LOCATION: 143..667
79      (ix) FEATURE:
80          (A) NAME/KEY: sig_peptide
81          (B) LOCATION: 143..199
83      (ix) FEATURE:
84          (A) NAME/KEY: mat_peptide
85          (B) LOCATION: 200..667
88      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
90 TCGGCAAAGC AGCCGGATAC CGCTACGTAT CTTGAAGTAT TGAAAATATT ACGATGCAAA 60
92 AAAGAAAATT TAAGTATAAT ACAGCAGGAT TCTTTAACGG ATTCTTAACA ATTTTCTTAA 120
94 CTGACCATAA AGGAACCAAA AT ATG AAA AAA GCA CTT GCC ACA CTG ATT GCC 172
95          Met Lys Lys Ala Leu Ala Thr Leu Ile Ala
96          -19          -15          -10
98 CTC GCT CTC CCG GCC GCC GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC 220
99 Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr
100          -5          1          5
102 GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA GGT TCT 268
103 Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly Ser
104          10          15          20
106 GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC 316
107 Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp
108          25          30          35
110 CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA 364
111 Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro
112          40          45          50          55
114 TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC 412
115 Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp
116          60          65          70
118 TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC 460
119 Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser
120          75          80          85
122 CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC AGC CAA 508
123 Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln
124          90          95          100
126 ACC TCC ATC GGC CTC GGC GTA TTG ACG GGC GTA AGC TAT GCC GTT ACC 556
127 Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr Ala Val Thr
128          105          110          115
130 CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA 604
131 Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys

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132 120          125          130          135
134 GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GTC GGC GTG 652
135 Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val
136          140          145          150
138 CGC GTC AAA TTC TGATATGCGC CTTATTCTGC AAACCGCCGA GCCTTCGGCG 704
139 Arg Val Lys Phe
140          155
142 GTTTTGT TTTT CTGCCACCGC AACTACACAA GCCGGCGGTT TTGTACGATA ATCCCGAATG 764
144 CTGCGGCTTC TGCCGCCCTA TTTTGTGAGG AATCCGAAAT GTCCAAAACC ATCATCCACA 824
146 CCGACA 830

```

149 (2) INFORMATION FOR SEQ ID NO: 2:

151 (i) SEQUENCE CHARACTERISTICS:

152 (A) LENGTH: 174 amino acids

153 (B) TYPE: amino acid

154 (D) TOPOLOGY: linear

156 (ii) MOLECULE TYPE: protein

158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

160 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala
161 -19          -15          -10          -5
163 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
164          1          5          10
166 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
167          15          20          25
169 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
170 30          35          40          45
172 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
173          50          55          60
175 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
176          65          70          75
178 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
179          80          85          90
181 Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly
182          95          100          105
184 Val Leu Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
185 110          115          120          125
187 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
188          130          135          140
190 Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe
191          145          150          155

```

194 (2) INFORMATION FOR SEQ ID NO: 3:

196 (i) SEQUENCE CHARACTERISTICS:

197 (A) LENGTH: 710 base pairs

198 (B) TYPE: nucleic acid

199 (C) STRANDEDNESS: double

200 (D) TOPOLOGY: linear

202 (ii) MOLECULE TYPE: DNA (genomic)

204 (iii) HYPOTHETICAL: NO

206 (iv) ANTI-SENSE: NO

208 (vi) ORIGINAL SOURCE:

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```

209      (A) ORGANISM: Neisseria meningitidis
210      (B) STRAIN: MCH88
212      (ix) FEATURE:
213          (A) NAME/KEY: CDS
214          (B) LOCATION: 116..643
216      (ix) FEATURE:
217          (A) NAME/KEY: sig_peptide
218          (B) LOCATION: 116..172
220      (ix) FEATURE:
221          (A) NAME/KEY: mat_peptide
222          (B) LOCATION: 173..643
225      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
227 GTATCTTGAG GCATTGAAAA TATTACAATG CAAAAAGAAA ATTTCAAGTAT AATACGGCAG 60
229 GATTCTTTAA CGGATTCTTA ACCATTTTTC TCCCTGACCA TAAAGGAATC AAGAT ATG 118
230                                     Met
231                                     -19
233 AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCC CTC CCG GCC GCC GCA 166
234 Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala Ala
235      -15                               -10                               -5
237 CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA CAC 214
238 Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His
239      1                               5                               10
241 GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG CGC 262
242 Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg
243 15                               20                               25                               30
245 ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT TAC 310
246 Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr
247      35                               40                               45
249 ACG CGC TAC AAA AAC TAT AAA CAA GTC CCA TCC ACC GAT TTC AAA CTT 358
250 Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu
251      50                               55                               60
253 TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC TTC GAC ACC CAA TCC CCC 406
254 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
255      65                               70                               75
257 GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC CTC AAC CGC GCC TCC GTC 454
258 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
259      80                               85                               90
261 GAC TTT AAC GGC AGC GAC TTC AGC CAA ACC TCC ACC GGC CTC GGC 502
262 Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly
263 95                               100                               105                               110
265 GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT 550
266 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
267      115                               120                               125
269 GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA GTC AAC ACT GTC AAA AAT 598
270 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
271      130                               135                               140
273 GTC CGT TCC GGC GAA CTG TCC GCC GGC GTA CGC GTC AAA TTC TGATATACGC 650
274 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
275      145                               150                               155

```

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277 GTTATTCCGC AAACCGCCGA GCCTTTCGGC GGTTTTGTTT TCCGCCGCCG CAACTACACA 710

281 (2) INFORMATION FOR SEQ ID NO: 4:

283 (i) SEQUENCE CHARACTERISTICS:

284 (A) LENGTH: 175 amino acids

285 (B) TYPE: amino acid

286 (D) TOPOLOGY: linear

288 (ii) MOLECULE TYPE: protein

290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

292 Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala

293 -19 -15 -10 -5

295 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala

296 1 5 10

298 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro

299 15 20 25

301 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp

302 30 35 40 45

304 Tyr Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys

305 50 55 60

307 Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser

308 65 70 75

310 Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser

311 80 85 90

313 Val Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu

314 95 100 105

316 Gly Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu

317 110 115 120 125

319 Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys

320 130 135 140

322 Asn Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe

323 145 150 155

326 (2) INFORMATION FOR SEQ ID NO: 5:

328 (i) SEQUENCE CHARACTERISTICS:

329 (A) LENGTH: 850 base pairs

330 (B) TYPE: nucleic acid

331 (C) STRANDEDNESS: double

332 (D) TOPOLOGY: linear

334 (ii) MOLECULE TYPE: DNA (genomic)

336 (iii) HYPOTHETICAL: NO

338 (iv) ANTI-SENSE: NO

340 (vi) ORIGINAL SOURCE:

341 (A) ORGANISM: Neisseria meningitidis

342 (B) STRAIN: Z4063

344 (ix) FEATURE:

345 (A) NAME/KEY: CDS

346 (B) LOCATION: 208..732

348 (ix) FEATURE:

349 (A) NAME/KEY: sig\_peptide

350 (B) LOCATION: 208..264

352 (ix) FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/684,883

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Input Set : N:\Crf3\RULE60\09684883.raw  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:30; Xaa Pos.7,73,126

## VERIFICATION SUMMARY

DATE: 07/30/2002

PATENT APPLICATION: US/09/684,883

TIME: 14:21:01

Input Set : N:\Crf3\RULE60\09684883.raw

Output Set: N:\CRF3\07302002\I684883.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:1050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0

L:1062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:64

L:1071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:112